

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/964,858C  
Source: 1Fw/6  
Date Processed by STIC: 6/15/06

***ENTERED***



IFW16

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/09/964,858C

**DATE:** 06/15/2006  
**TIME:** 09:26:40

**Input Set :** A:\P07274US02\_Sequence.txt  
**Output Set:** N:\CRF4\06152006\I964858C.raw

3 <110> APPLICANT: HOSTETTER, Margaret K.  
4 DEVORE-CARTER, Denise  
6 <120> TITLE OF INVENTION: ANTIBODIES TO THE PROPEPTIDE OF CANDIDA ALBICANS  
8 <130> FILE REFERENCE: P07274US02/BAS  
10 <140> CURRENT APPLICATION NUMBER: US 09/964,858C  
11 <141> CURRENT FILING DATE: 2001-09-28  
13 <150> PRIOR APPLICATION NUMBER: US 60/237,082  
14 <151> PRIOR FILING DATE: 2000-09-28  
16 <160> NUMBER OF SEQ ID NOS: 13  
18 <170> SOFTWARE: PatentIn version 3.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 1664  
22 <212> TYPE: PRT  
23 <213> ORGANISM: Candida albicans  
25 <400> SEQUENCE: 1  
27 Met Asn Ser Thr Pro Ser Lys Leu Leu Pro Ile Asp Lys His Ser His  
28 1 5 10 15  
31 Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro  
32 20 25 30  
35 Thr Lys Pro Leu Asn Phe Pro Arg Thr Asn Ser Lys Pro Ser Leu Asp  
36 35 40 45  
39 Pro Asn Ser Ser Ser Asp Thr Tyr Thr Ser Glu Gln Asp Gln Glu Lys  
40 50 55 60  
43 Gly Lys Glu Glu Lys Lys Asp Thr Ala Phe Gln Thr Ser Phe Asp Arg  
44 65 70 75 80  
47 Asn Phe Asp Leu Asp Asn Ser Ile Asp Ile Gln Gln Thr Ile Gln His  
48 85 90 95  
51 Gln Gln Gln Pro Gln Gln Gln Gln Leu Ser Gln Thr Asp Asn  
52 100 105 110  
55 Asn Leu Ile Asp Glu Phe Ser Phe Gln Thr Pro Met Thr Ser Thr Leu  
56 115 120 125  
59 Asp Leu Thr Lys Gln Asn Pro Thr Val Asp Lys Val Asn Glu Asn His  
60 130 135 140  
63 Ala Pro Thr Tyr Ile Asn Thr Ser Pro Asn Lys Ser Ile Met Lys Lys  
64 145 150 155 160  
67 Ala Thr Pro Lys Ala Ser Pro Lys Lys Val Ala Phe Thr Val Thr Asn  
68 165 170 175  
71 Pro Glu Ile His His Tyr Pro Asp Asn Arg Val Glu Glu Glu Asp Gln  
72 180 185 190  
75 Ser Gln Gln Lys Glu Asp Ser Val Glu Pro Pro Leu Ile Gln His Gln  
76 195 200 205  
79 Trp Lys Asp Pro Ser Gln Phe Asn Tyr Ser Asp Glu Asp Thr Asn Ala  
80 210 215 220

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83 Ser Val Pro Pro Thr Pro Pro Leu His Thr Thr Lys Pro Thr Phe Ala
84 225          230          235          240
87 Gln Leu Leu Asn Lys Asn Asn Glu Val Asn Ser Glu Pro Glu Ala Leu
88          245          250          255
91 Thr Asp Met Lys Leu Lys Arg Glu Asn Phe Ser Asn Leu Ser Leu Asp
92          260          265          270
95 Glu Lys Val Asn Leu Tyr Leu Ser Pro Thr Asn Asn Asn Ser Lys
96          275          280          285
99 Asn Val Ser Asp Met Asp Ser His Leu Gln Asn Leu Gln Asp Ala Ser
100         290         295         300
103 Lys Asn Lys Thr Asn Glu Asn Ile His Asn Leu Ser Phe Ala Leu Lys
104 305          310          315          320
107 Ala Pro Lys Asn Asp Ile Glu Asn Pro Leu Asn Ser Leu Thr Asn Ala
108          325          330          335
111 Asp Ile Ser Leu Arg Ser Ser Gly Ser Ser Gln Ser Ser Leu Gln Ser
112          340          345          350
115 Leu Arg Asn Asp Asn Arg Val Leu Glu Ser Val Pro Gly Ser Pro Lys
116          355          360          365
119 Lys Val Asn Pro Gly Leu Ser Leu Asn Asp Gly Ile Lys Gly Phe Ser
120          370          375          380
123 Asp Glu Val Val Glu Ser Leu Leu Pro Arg Asp Leu Ser Arg Asp Lys
124 385          390          395          400
127 Leu Glu Thr Thr Lys Glu His Asp Ala Pro Glu His Asn Asn Glu Asn
128          405          410          415
131 Phe Ile Asp Ala Lys Ser Thr Asn Thr Asn Lys Gly Gln Leu Leu Val
132          420          425          430
135 Ser Ser Asp Asp His Leu Asp Ser Phe Asp Arg Ser Tyr Asn His Thr
136          435          440          445
139 Glu Gln Ser Ile Leu Asn Leu Leu Asn Ser Ala Ser Gln Ser Gln Ile
140          450          455          460
143 Ser Leu Asn Ala Leu Glu Lys Gln Arg Gln Thr Gln Glu Gln Glu Gln
144 465          470          475          480
147 Thr Gln Ala Ala Glu Pro Glu Glu Glu Thr Ser Phe Ser Asp Asn Ile
148          485          490          495
151 Lys Val Lys Gln Glu Pro Lys Ser Asn Leu Glu Phe Val Lys Val Thr
152          500          505          510
155 Ile Lys Lys Glu Pro Val Ser Ala Thr Glu Ile Lys Ala Pro Lys Arg
156          515          520          525
159 Glu Phe Ser Ser Arg Ile Leu Arg Ile Lys Asn Glu Asp Glu Ile Ala
160          530          535          540
163 Glu Pro Ala Asp Ile His Pro Lys Lys Glu Asn Glu Ala Asn Ser His
164 545          550          555          560
167 Val Glu Asp Thr Asp Ala Leu Leu Lys Lys Ala Leu Asn Asp Asp Glu
168          565          570          575
171 Glu Ser Asp Thr Thr Gln Asn Ser Thr Lys Met Ser Ile Arg Phe His
172          580          585          590
175 Ile Asp Ser Asp Trp Lys Leu Glu Asp Ser Asn Asp Gly Asp Arg Glu
176          595          600          605
179 Asp Asn Asp Asp Ile Ser Arg Phe Glu Lys Ser Asp Ile Leu Asn Asp

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180	610	615	620
183	Val Ser Gln Thr Ser Asp Ile Ile Gly Asp Lys Tyr Gly Asn Ser Ser		
184	625	630	635
187	Ser Glu Ile Thr Thr Lys Thr Leu Ala Pro Pro Arg Ser Asp Asn Asn		640
188	645	650	655
191	Asp Lys Glu Asn Ser Lys Ser Leu Glu Asp Pro Ala Asn Asn Glu Ser		
192	660	665	670
195	Leu Gln Gln Gln Leu Glu Val Pro His Thr Lys Glu Asp Asp Ser Ile		
196	675	680	685
199	Leu Ala Asn Ser Ser Asn Ile Ala Pro Pro Glu Glu Leu Thr Leu Pro		
200	690	695	700
203	Val Val Glu Ala Asn Asp Tyr Ser Ser Phe Asn Asp Val Thr Lys Thr		
204	705	710	715
207	Phe Asp Ala Tyr Ser Ser Phe Glu Glu Ser Leu Ser Arg Glu His Glu		720
208	725	730	735
211	Thr Asp Ser Lys Pro Ile Asn Phe Ile Ser Ile Trp His Lys Gln Glu		
212	740	745	750
215	Lys Gln Lys Lys His Gln Ile His Lys Val Pro Thr Lys Gln Ile Ile		
216	755	760	765
219	Ala Ser Tyr Gln Gln Tyr Lys Asn Glu Gln Glu Ser Arg Val Thr Ser		
220	770	775	780
223	Asp Lys Val Lys Ile Pro Asn Ala Ile Gln Phe Lys Lys Phe Lys Glu		
224	785	790	795
227	Val Asn Val Met Ser Arg Arg Val Val Ser Pro Asp Met Asp Asp Leu		800
228	805	810	815
231	Asn Val Ser Gln Phe Leu Pro Glu Leu Ser Glu Asp Ser Gly Phe Lys		
232	820	825	830
235	Asp Leu Asn Phe Ala Asn Tyr Ser Asn Asn Thr Asn Arg Pro Arg Ser		
236	835	840	845
239	Phe Thr Pro Leu Ser Thr Lys Asn Val Leu Ser Asn Ile Asp Asn Asp		
240	850	855	860
243	Pro Asn Val Val Glu Pro Pro Glu Pro Lys Ser Tyr Ala Glu Ile Arg		
244	865	870	875
247	Asn Ala Arg Arg Leu Ser Ala Asn Lys Ala Ala Pro Asn Gln Ala Pro		880
248	885	890	895
251	Pro Leu Pro Pro Gln Arg Gln Pro Ser Ser Thr Arg Ser Asn Ser Asn		
252	900	905	910
255	Lys Arg Val Ser Arg Phe Arg Val Pro Thr Phe Glu Ile Arg Arg Thr		
256	915	920	925
259	Ser Ser Ala Leu Ala Pro Cys Asp Met Tyr Asn Asp Ile Phe Asp Asp		
260	930	935	940
263	Phe Gly Ala Gly Ser Lys Pro Thr Ile Lys Ala Glu Gly Met Lys Thr		
264	945	950	955
267	Leu Pro Ser Met Asp Lys Asp Asp Val Lys Arg Ile Leu Asn Ala Lys		960
268	965	970	975
271	Lys Gly Val Thr Gln Asp Glu Tyr Ile Asn Ala Lys Leu Val Asp Gln		
272	980	985	990
275	Lys Pro Lys Lys Asn Ser Ile Val Thr Asp Pro Glu Asp Arg Tyr Glu		
276	995	1000	1005

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279 Glu Leu Gln Gln Thr Ala Ser Ile His Asn Ala Thr Ile Asp Ser  
 280 1010 1015 1020  
 283 Ser Ile Tyr Gly Arg Pro Asp Ser Ile Ser Thr Asp Met Leu Pro  
 284 1025 1030 1035  
 287 Tyr Leu Ser Asp Glu Leu Lys Lys Pro Pro Thr Ala Leu Leu Ser  
 288 1040 1045 1050  
 291 Ala Asp Arg Leu Phe Met Glu Gln Glu Val His Pro Leu Arg Ser  
 292 1055 1060 1065  
 295 Asn Ser Val Leu Val His Pro Gly Ala Gly Ala Ala Thr Asn Ser  
 296 1070 1075 1080  
 299 Ser Met Leu Pro Glu Pro Asp Phe Glu Leu Ile Asn Ser Pro Ala  
 300 1085 1090 1095  
 303 Arg Asn Val Ser Asn Asn Ser Asp Asn Val Ala Ile Ser Gly Asn  
 304 1100 1105 1110  
 307 Ala Ser Thr Ile Ser Phe Asn Gln Leu Asp Met Asn Phe Asp Asp  
 308 1115 1120 1125  
 311 Gln Ala Thr Ile Gly Gln Lys Ile Gln Glu Gln Pro Ala Ser Lys  
 312 1130 1135 1140  
 315 Ser Ala Asn Thr Val Arg Gly Asp Asp Asp Gly Leu Ala Ser Ala  
 316 1145 1150 1155  
 319 Pro Glu Thr Pro Arg Thr Pro Thr Lys Lys Glu Ser Ile Ser Ser  
 320 1160 1165 1170  
 323 Lys Pro Ala Lys Leu Ser Ser Ala Ser Pro Arg Lys Ser Pro Ile  
 324 1175 1180 1185  
 327 Lys Ile Gly Ser Pro Val Arg Val Ile Lys Lys Asn Gly Ser Ile  
 328 1190 1195 1200  
 331 Ala Gly Ile Glu Pro Ile Pro Lys Ala Thr His Lys Pro Lys Lys  
 332 1205 1210 1215  
 335 Ser Phe Gln Gly Asn Glu Ile Ser Asn His Lys Val Arg Asp Gly  
 336 1220 1225 1230  
 339 Gly Ile Ser Pro Ser Ser Gly Ser Glu His Gln Gln His Asn Pro  
 340 1235 1240 1245  
 343 Ser Met Val Ser Val Pro Ser Gln Tyr Thr Asp Ala Thr Ser Thr  
 344 1250 1255 1260  
 347 Val Pro Asp Glu Asn Lys Asp Val Gln His Lys Pro Arg Glu Lys  
 348 1265 1270 1275  
 351 Gln Lys Gln Lys His His His Arg His His His His His His Lys  
 352 1280 1285 1290  
 355 Gln Lys Thr Asp Ile Pro Gly Val Val Asp Asp Glu Ile Pro Asp  
 356 1295 1300 1305  
 359 Val Gly Leu Gln Glu Arg Gly Lys Leu Phe Phe Arg Val Leu Gly  
 360 1310 1315 1320  
 363 Ile Lys Asn Ile Asn Leu Pro Asp Ile Asn Thr His Lys Gly Arg  
 364 1325 1330 1335  
 367 Phe Thr Leu Thr Leu Asp Asn Gly Val His Cys Val Thr Thr Pro  
 368 1340 1345 1350  
 371 Glu Tyr Asn Met Asp Asp His Asn Val Ala Ile Gly Lys Glu Phe  
 372 1355 1360 1365  
 375 Glu Leu Thr Val Ala Asp Ser Leu Glu Phe Ile Leu Thr Leu Lys

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376	1370	1375	1380	
379	Ala Ser	Tyr Glu Lys Pro Arg	Gly Thr Leu Val Glu	Val Thr Glu
380	1385	1390	1395	
383	Lys Lys	Val Val Lys Ser Arg	Asn Arg Leu Ser Arg	Leu Phe Gly
384	1400	1405	1410	
387	Ser Lys	Asp Ile Ile Thr Thr	Thr Lys Phe Val Pro	Thr Glu Val
388	1415	1420	1425	
391	Lys Asp	Thr Trp Ala Asn Lys	Phe Ala Pro Asp Gly	Ser Phe Ala
392	1430	1435	1440	
395	Arg Cys	Tyr Ile Asp Leu Gln	Gln Phe Glu Asp Gln	Ile Thr Gly
396	1445	1450	1455	
399	Lys Ala	Ser Gln Phe Asp Leu	Asn Cys Phe Asn Glu	Trp Glu Thr
400	1460	1465	1470	
403	Met Ser	Asn Gly Asn Gln Pro	Met Lys Arg Gly Lys	Pro Tyr Lys
404	1475	1480	1485	
407	Ile Ala	Gln Leu Glu Val Lys	Met Leu Tyr Val Pro	Arg Ser Asp
408	1490	1495	1500	
411	Pro Arg	Glu Ile Leu Pro Thr	Ser Ile Arg Ser Ala	Tyr Glu Ser
412	1505	1510	1515	
415	Ile Asn	Glu Leu Asn Asn Glu	Gln Asn Asn Tyr Phe	Glu Gly Tyr
416	1520	1525	1530	
419	Leu His	Gln Glu Gly Gly Asp	Cys Pro Ile Phe Lys	Lys Arg Phe
420	1535	1540	1545	
423	Phe Lys	Leu Met Gly Thr Ser	Leu Leu Ala His Ser	Glu Ile Ser
424	1550	1555	1560	
427	His Lys	Thr Arg Ala Lys Ile	Asn Leu Ser Lys Val	Val Asp Leu
428	1565	1570	1575	
431	Ile Tyr	Val Asp Lys Glu Asn	Ile Asp Arg Ser Asn	His Arg Asn
432	1580	1585	1590	
435	Phe Ser	Asp Val Leu Leu Leu	Asp His Ala Phe Lys	Ile Lys Phe
436	1595	1600	1605	
439	Ala Asn	Gly Glu Leu Ile Asp	Phe Cys Ala Pro Asn	Lys His Glu
440	1610	1615	1620	
443	Met Lys	Ile Trp Ile Gln Asn	Leu Gln Glu Ile Ile	Tyr Arg Asn
444	1625	1630	1635	
447	Arg Phe	Arg Arg Gln Pro Trp	Val Asn Leu Met Leu	Gln Gln Gln
448	1640	1645	1650	
451	Gln Gln	Gln Gln Gln Gln Gln	Ser Ser Gln Gln	
452	1655	1660		
455	<210>	SEQ ID NO: 2		
456	<211>	LENGTH: 5194		
457	<212>	TYPE: DNA		
458	<213>	ORGANISM: Candida albicans		
460	<400>	SEQUENCE: 2		
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463	ttaatttta	ataaagaatc agtagatcta	ttgttaaaag aaatgaactc aactccaagt	120
465	aaatttattac	cgtatgataaa acattctcat	ttacaattac agcctcaatc gtctcgcc	180
467	tcaatattta	attccccaaac aaaaccattg	aattccccaa gaccaaattc caagccgagt	240
469	ttagatccaa	attcaagctc tgatacac	actagcgaac aagatcaaga gaaaggaaa	300

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 06/15/2006  
PATENT APPLICATION: US/09/964,858C                    TIME: 09:26:41

Input Set : A:\P07274US02\_Sequence.txt  
Output Set: N:\CRF4\06152006\I964858C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 3

**VERIFICATION SUMMARY**

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Input Set : A:\P07274US02\_Sequence.txt

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L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0